

LDA (Linear Discriminant Analysis)

- LDA or Normal Discriminant Analysis (NDA) or Discriminant Function Analysis (DFA) is a dimensionality reduction technique which is commonly used for supervised classification problems.
- It is used for modeling differences in groups i.e., separating two or more classes. It is used to project the feature in higher dimension space into lower dimension space.
- For example, we have two classes and we need to separate them efficiently. Classes can have multiple features. Using only a single feature to classify them may result in some overlapping datapoints. So we will keep on increasing the number of features for proper classification.

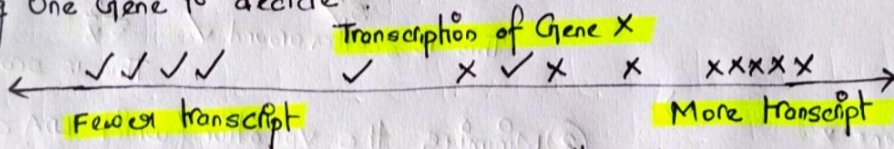
Example

→ We got a cancer drug, → It works great for some people
→ But for many, it make them feel worse.

So how to decide who to give the drug to?

Therefore let's use feature of the drug, Gene.

Using One Gene to decide.



✓ → Drugs works & X → Drugs don't work

For most part on left side, drugs works in people with low transcription of Gene X.

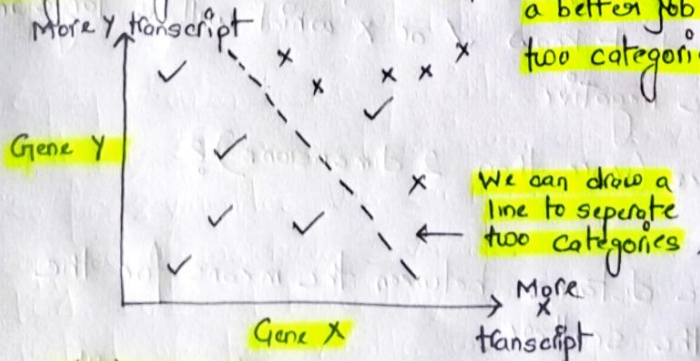
And most part on Right side, drugs does not work in people with high transcription of Gene X.

In middle, there is overlap and no obvious "cutoff" for who to give the drug to.

In summary, Gene X does an OK job at telling us who should/shouldn't take the drug.

Using two gene to decide, Inference - two genes does a better job separating two categories.

So for plotting 3 variable, we can plot 2D plot.



✓ → Drug works

X → Drugs don't work

But what if we need four (or more) gene to separate two categories?

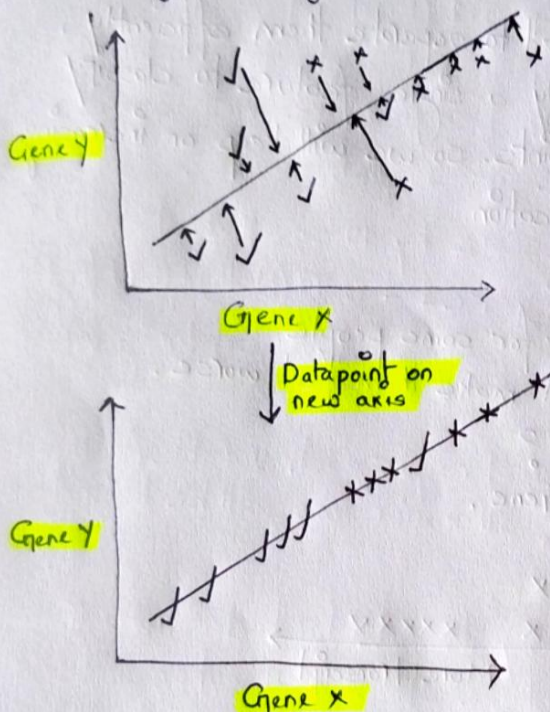
So we use dimensionality reduction technique LDA which is like PCA, but it focus on maximizing the separability among known categories.

- PCA is useful for plotting data with a lots of dimension onto a simple x/y plot.

- However, LDA is not interested in genes with most variation instead LDA interest is maximizing the separability between the two groups/known categories.

So how LDA work?

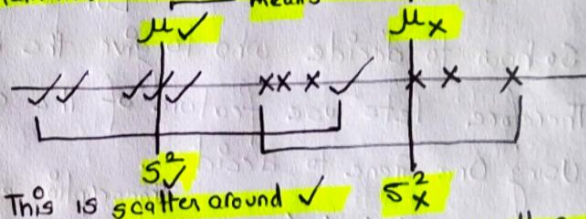
Reducing a 2D graph to 1D graph with LDA.



- LDA uses both genes to create new axis.
- It projects the data onto new axis in a way to maximize the separation of the two categories.

- So LDA create a new axis and project the data on the new axis that maximize the separation between two categories.

① Maximize the distance between means.



This is scatter around ✓

This is scatter around x

② Minimize the variation (which LDA called scatter and is represented by $s_✓^2$ and s_x^2) within each category.

→ Normally, we construct low dimensional space which maximize the between class variance & minimize the within class variance.

So the new axis is created based on ① and ② criteria simultaneously.

In short, by formula given by

$\mu_✓ - \mu_x \rightarrow$ Between Class Variance.

$s_✓^2 + s_x^2 \rightarrow$ Within Class Variance.

$$\frac{(\mu_✓ - \mu_x)^2}{s_✓^2 + s_x^2} \rightarrow \frac{\text{Ideally large}}{\text{Ideally small}} = \frac{d^2}{s_✓^2 + s_x^2}$$

we can also write eqn as

It is the ratio between two mean squared over the sum of the scattered. Numerator is squared because we don't know ✓ or x which will be large and we don't want the output to be negative.

③ What if we have more than 2 genes (more than 2 dimensions)?

→ The process is same.

Create an axis that maximize the distance between the means for the two categories while minimizing the scatter.

→ LDA is like PCA both try to reduce dimensions, but PCA looks at genes with most variation but LDA tries to maximize the separation of known categories.